



**Figure 1:**  
**Delta-6 Desaturase Sequence Alignment:**  
**Consensus key** (see documentation for details)  
\* - single, fully conserved residue  
: - conservation of strong groups  
. - conservation of weak groups  
- no consensus

CLUSTAL W (1.81) multiple sequence alignment

Mucor-D6	-----
Rhizopus-D6	-----
Malpina-D6	-----
<b>Sdiclina-D6</b>	-----
Phytium-D6	-----
Phaeo-D6	-----
Physcomit-D6	MVFAGGGLQGSLEENIDVEHIASMSLFSDFFSYVSSVGSWSVHSIQPLKRLTSKKRVS
Ceratodon-D6	MVSQGGGLSQGSIEENIDVEHLATMPLVSDFLNVLGLTTLGQWSLSTTFAFKRLTTKKHSS
C.elegansD6	-----
Borage-D6	-----
Human-D6	-----
Mucor-D6	-----MSSDVGATVPHFYTRAEIADIHQDV-----L-DKKPEAR
Rhizopus-D6	-----MSTSDRQSV-----FTLKELELINQKH-----R-DGDKSAMK
Malpina-D6	-----MAAAPSVRT-----FTRAEIILNAEALN-----EGKKDAEAPF



Phytium-D6	-----ETSKAEIEGEPASDEERARRINEFIASYRRLRVKVGMLYDASALYYAWKL
Phaeo-D6	-----PETTGKEPQQ-----IAFEKGYRDLRSKLIMMGFKSNKWFYVYKC
Physcomit-D6	-----RVEPTP-----ELLKDFREMRALFLREQLFKSSKLYYVMKL
Ceratodon-D6	-----REEPTL-----ELLKEYRELRALFLREQLFKSSKSYLFKT
C.elegansD6	DEFLEKQLEKRLDKVDINVSAYDVSVAQEKKMVESFEKLRQKLHDDGLMKANETYFLFKA
Borage-D6	-----KDYSVS-----EVSKDYRKLVFEFSKMGLYDKKGHIMFATL
Human-D6	P-----EEPSQDHGKN-----SKITEDFRALRKTAEDMNLFKTNHVFFLLLL

Mucor-D6	STTLVCIVGLAILKAWGRESTLAVFIAASLVGLFWQCGWLAHDYAHYQVIKDPNVNNL
Rhizopus-D6	LSTLALCAAGLTLLYAYGHTSTLAVVASAIIVGIFWQCGWLAHDFGHHQCFFEDRSWNDV
Malpina-D6	SNLCIWGLSTFIVAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHHQVFQDRFWGDL
<b>Sdiclina-D6</b>	ASTLSIALVSAACLHFD--STAMYMVAAVILGLFYQCGWLAHDFLHHQVFENHLFGDL
Phytium-D6	VSTFGIAVLMAICFFFN--SFAMYMVAGVIMGLFYQCGWLAHDFLHNQVCENRTLGNL
Phaeo-D6	LSNMAIWAACALVFYSD--RFVWHLASAVMLGTFQCGWLAHDFLHHQVFTKRKHGDL
Physcomit-D6	LTNVAIFAASIAIICWSK--TISAVLASACMMALCFQCGWLSHDFLHNQVFETRNLNEV
Ceratodon-D6	LINVSIVATSIASISLYK--SYRAVLLSASLMGLFIQCGWLSHDFLHHQVFETRNLNDV
C.elegansD6	ISTLSIMAFAFYLYLG-----WYITSACLLALAWQQFGWLTHEFCHQOQPTKNRPLNDT
Borage-D6	CFIAMLFAMSVYGVLFCEG--VIVHLFSGCLMGFLWISQGWIGHDAGHYMVVSDSRLNKE
Human-D6	AHIIALESIAWFTVFYFGN-GWIPTLITAFVLATSQAQAGWLQHDYGHLSVYRKPKWNHL

Mucor-D6	FLVTFGNLVQGFSLSWWKNKHNTHHASTNVSGE-----DPDIDTAPILLWDEFAVANE
Rhizopus-D6	LVVFLGNFCQGFSLSWWKNKHNTHHASTNVHGH-----DPDIDTAPVLLWDEYASAA
Malpina-D6	FGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGE-----DPDIDTHPLLTWSEHALEME
<b>Sdiclina-D6</b>	VGVMVGNLWQGFVSQWWKNKHNTHHAI PNLHATPEIAFHGDPDIDTMPILAWSLKMAQ--
Phytium-D6	IGCLVGNAWQGFVSQWWKNKHNHLHHA VPNLHSAKDEGFIGDPDIDTMPILLAWSKEMAR--



Physcomit-D6	R-----LLEKGTVLPHYFWFVGTAACYLLP--GWKPLVWMAVTELMMSGMLLGFVFLSH
Ceratodon-D6	K-----LLERGTMALHYIWFNSVAFYLLP--GWKPVVWVMVSELMSGFLLGYYFVFLSH
C.elegansD6	YKVYQRNAFWEQATIVGHWAWVFYQLFLLPT--WPLRVAYFIIISQMGGLLIAHVVTFNH
Borage-D6	-KRNVSYRAHELGLCLVFSIWYPLLVSCLPN---WGERIMFVIASLSVTGMQVQVQFSLNH
Human-D6	---IVHKNWVDLAWAVSYIIRFFITYIPFYG--ILGALLFLNFIRFLESHWFVWVTQMNH
	: . : .. *
Mucor-D6	NGMPVYSPEEАНHTEFYELQCITGRDVN-----CTVFGDWLMGGLNYQIEHHLFPEMPRH
Rhizopus-D6	NGMPVITEEKAESMEFFEIQVITGRDVT-----LSPLGDWFMGGLNYQIEHHVFPNMPRH
Malpina-D6	NGMPVISKEEAVDMDFFTKQIITGRDVH-----PGLFANWFTGGLNYQIEHHLFPSPMPRH
<b>Sdiclina-D6</b>	NGMEVFDKD--SKPDFWKQLQVLSTRNV-----SSLIWDWFMGGLNYQIDHHLFPMVPRH
Phytium-D6	NGMSVYERE--TKPDFWQLQVTTTRNIR-----ASVMDWFTGGLNYQIDHHLFPLVPRH
Phaeo-D6	NGMATYNAD--ARPDFWKQLQVTTTRNVTTGGHGFPAQVDFWFCGGLQYQVDDHHLFPSLPRH
Physcomit-D6	NGMEVYN-----SSKEFVSAQIVSTRDIK-----GNIFNDWFTGGLNRQIEHHLFPTMPRH
Ceratodon-D6	NGMEVYN-----TSKDFVNAQIASTRDIK-----AGVNDWFTGGLNRQIEHHLFPTMPRH
C.elegansD6	NSVDKYPANSRILNNFAALQILTTTRNMT-----PSPFIDWLWGGLNYQIEHHLFPTMPRC
Borage-D6	FSSSVYVGK-PKGNWFEKQTDGTLDIS-----CPPWMDWFHGGGLQFQIEHHLFPKMPC
Human-D6	IVMEIDQEA---YRDWFSSQLTATCNVE-----QSFNDWFSGHLNFQIEHHLFPTMPRH
	:: * : : * * : * : * : * : *
Mucor-D6	HL SKVKSMVKPIAQKYNIPYHDTTVIGGTIEVLQTLDFVQ-----KISQKFSKKML-----
Rhizopus-D6	NLPKVKPMVKSCLKKYDINYHDTGFLKGTLEVLKTLDIS-----KLSLQLSKKSF-----
Malpina-D6	NFSKIQPAVETLCKKYGVRYHTTGMIEGTAEVFSRLNEVS-----KAASKMGKAQ-----
<b>Sdiclina-D6</b>	NLPALNVLVKSLCKQYDIPYHETGFIAGMAEVVHLERIS-----IEFFKEFPAM-----
Phytium-D6	NLPKVNVLKSLCKEFDIPFHETGFWEGLYEVVDHLADIS-----KEFITTEFPAM-----
Phaeo-D6	NLAKTHALVESFCKEWGVQYHEADLVDTGMEVLHHLGSAGEFVVDVFRDGPAM-----
Physcomit-D6	NLNKIAPRVEVFCCKHGLVYEDVSIATGTCKVLKALKEVAE---AAAEQHATTS-----

Ceratodon-D6	NLNKISPHVETLCKKHGLVYEDVSMASGTYRVLKTLKDVAD---	AASHQQLAAS-----
C.elegansD6.	NLNACVKYVKEWCKENNLPLYLVDDYFDGYAMNLQQLKNMA-----	EHIQAKAA-----
Borage-D6	NLRKISPYVIELCKKHNLPTYNYASFSSKANEMTLRTRLRNTALQARDITKPLPKNLVWEALH	
Human-D6	NLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKSGKLWLDAYLHKNLLE-----	
	::: . . . . . *	
Mucor-D6	---	
Rhizopus-D6	---	
Malpina-D6	---	
<b>Sdiclina-D6</b>	---	
Phytium-D6	---	
Phaeo-D6	---	
Physcomit-D6	---	
Ceratodon-D6	---	
C.elegansD6	---	
Borage-D6	THG	
Human-D6	---	

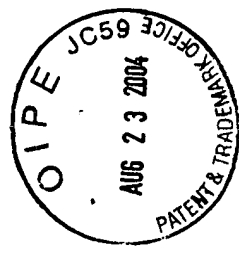


Figure 2:

Comparison of nucleotide sequence of *S. diclina*  $\Delta 6$ -desaturase versus *Pythium irregulare*  $\Delta 6$ -desaturase:

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	9148	Length:	1383
Ratio:	6.717	Gaps:	3
Percent Similarity:	68.948	Percent Identity:	68.948

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 5  
. = 1

*S. diclina*-D6 x *Pythium irregulare*-D6

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1 ATGGTCCAGGGGCAAAAAGGCCGAGAAAGATCTCG.....TGGGCGACCAT 44
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 ATGGTGGACCTCAAGCCTGGAGTGAAGCGCCTGGTGAGCTGGAAGGAGAT 50
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
45 CCGTGAGCACAAACCGCCAAAGACAAACGCGTGGATCGTGATCCACCAAGG 94
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 CCGCGAGCACGCGACGCCCGCGACCGCGTGGATCGTGATTCACCAAGG 100
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
95 TGTACGACATCTCGGCCTTTGAGGACCAACCGGGCGGCGTCGTCATGTTTC 144
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 TCTACGACATCTCCAAGTGGGACTCGCACCCGGGTGGCTCCGTCGATGCTC 150
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
145 ACGCAGGCCCGGGAAGACGCGACCGGATGCGTTCGCTTCCACCCGAG 194
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
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998 GCGTGGCATACTTCCTCATGGGCCAGGCGTCTCGGGCTTGCTCCTGGCG 1047

1030 ATGGTCTTTAGCGTCGGCCACAACGGCATGGAGGTCTTTGACAAGGACAG 1079
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1048 CTGGTGTTCAGTATTGGCCACAACGGCATGTCGGGTACGAGCGCGAAAC 1097

1080 CAAGCCCGATTTTTGAAGCTGCAAGTGCTCTCGACGCGCAACGTGACGT 1129
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1098 CAAGCCGGACTTCTGGCAGCTGCAGGTGACCACGACGCGCAACATCCGCG 1147

1130 CGTCGCTCTGGATCGACTGGTTTCATGGGGCGGCTCAAACTACCAGATCGAC 1179
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1148 CGTCGGTATTTCATGGACTGGTTTCACCGGTGGCTTGAACCTACCAGATCGAC 1197

1180 CACCACCTGTTCCTCCGATGGTGCCCCGGGCACAACCTCCCCGGCGCTCAACGT 1229
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1198 CATCACCTGTTCCTCCGCTCGTGCCCGGCCACAACCTGCCAAAAGGTCAACGT 1247

1230 GCTCGTCAAGTCGCTCTGCAAGCAGTACGACATCCCATAACCACGAGACGG 1279
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1248 GCTCATCAAGTCGCTATGCAAGGAGTTCGACATCCCCGTCCACGAGACCG 1297

1280 GCTTCATCGCGGGCATGGCCGAGGTGCTCGTGCACCTCGAGCGCATCTCG 1329
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1298 GCTTCTGGGAGGGCATCTACGAGGTGCTGGACCACCTGGCGGACATCAGC 1347

1330 ATCGAGTTCCTCAAGGAGTTTCCCGCCCATGTAA 1362
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1348 AAGGAATTTCATCACCAGATTCCCGAGCGGATGTAA 1380

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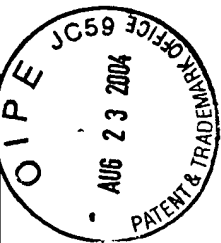


Figure 3:

Comparison of amino acid sequence of  $\Delta 6$ -desaturases from *S. diclina* and *P. irregulare*

Query= *S. diclina*  $\Delta 6$ -desaturase

Subject: *Pythium Irregulare*  $\Delta 6$ -desaturase

>gi|16033736|gb|AF419296.1|AF419296 *Pythium irregulare* delta-6 fatty acid desaturase  
mRNA, complete cds  
Length = 1380

Score = 548 bits (1412), Expect = e-154

**Identities = 267/449 (59%),** Positives = 328/449 (73%), Gaps = 5/449 (1%)

Frame = +1

Query: 10 ISWATIREHNRQDNAWIVIIHHKVYDISAFEDHPGGVVMFTQAGEDATDAFAVFPSSALK 69

+SW IREH AWIVIIHHKVYDIS ++ HPGG VM TQAGEDATDAFAVFPSSALK

Sbjct: 34 VSWKEIREHATPATAWIVIIHHKVYDISKWDSPGGSVMLTQAGEDATDAFAVFPSSALK 213

Query: 70 LLEQYVVGVDVDQSTAAV--DTSISDEVKKSQ---SDFIASYRKLRLEVKRXXXXXXXXXX 124

LLEQ+YVGVDVD+++ A SDE + + ++FIASYR+LR++VK

Sbjct: 214 LLEQFYVGVDVDETSKAEIEGEPASDEERARRERINEFIASYRRLRVKVGKMGGLYDASALY 393

Query: 125 XXXXCASLTSLIALVSAACICLHFDSTAMYMVAAILGLFYQQCGWLAHDFLHHQVFENHLF 184

ST IA++S AIC F+S AMYMVA VI+GLFYQQ GWLAHDFLH+QV EN

Sbjct: 394 YAWKLVSTFGIAVLMSAICFFFNFSFAMYMVAGVIMGLFYQQSGWLAHDFLHNQVCENRTL 573

Query: 185 GDLVGVVGNLWQGFVSQVWKNKHNTHHAIPNLHATPEIAFHGDPDIDTMPILAWSLKMA 244  
G+L+G +VGN WQGFVSQVWKNKHN HHA+PNLH+ + F GDPDIDTMP+LAWS +MA  
Sbjct: 574 GNLIGCLVGNWQGFVSQVWKNKHNHLHHAVPNLHSAKDEGFIGDPDIDTMPILLAWSKEMA 753

Query: 245 QHAVDSPVGLFFMRYQAYLYFPILLFARISWVIQSAMYAFYNVGPGETFDKVQYPLLERA 304  
+ A +S G FF+R QA+LYFP+LL AR+SW+ QS Y F G FDKV++ E+A  
Sbjct: 754 RKAFESAHGPFPIRNQAFLYFPILLARLSWLAQSFFYVFTFEFS-FGIFDKVEFDGPEKA 930

Query: 305 XXXXXXXXXXXXXAANMSLLQAAFLFVSQASCGFLAMVFSVGHNGMEVFDKDSKPDF 364  
NMSL + A+ + QASCGL LA+VFS+GHNGM V+++++KPDF  
Sbjct: 931 GLIVHYIWQLAIPYFCNMMSLFEQVAYFLMGQASCGLLALLVFSIGHNGMSVYERETKPDF 1110

Query: 365 WKLQVLSTRNVTSLSLWIDWFMGGLNYQIDHHLFPMVPRHNLPALNVLVKSLCKQYDIPYH 424  
W+LQV +TRN+ +S+++DWF GGLNYQIDHHLFP+VPRHNL +NVL+KSLCK++DIP+H  
Sbjct: 1111WQLQVTTTRNIRASVFMDFWTGGLNYQIDHHLFPLVPRHNLPKVNVLIKSLCKEFDIPFH 1290

Query: 425 ETGFIAGMAEVVHLEIRISIEFFEKEFPAM 453  
ETGF G+ EVV HL IS EF EFPAM  
Sbjct: 1291ETGFWEIGYEVVDHLADISKEFITEFPAM 1377